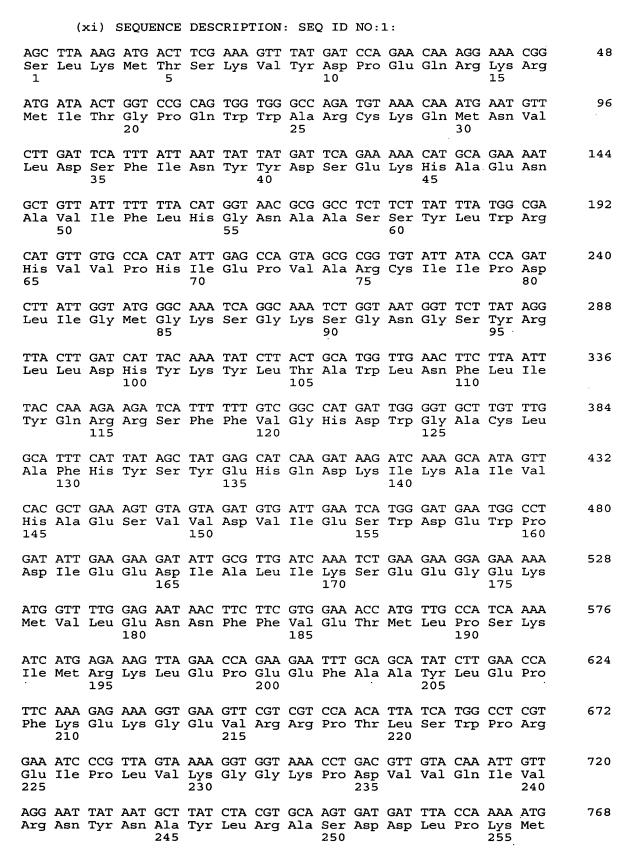
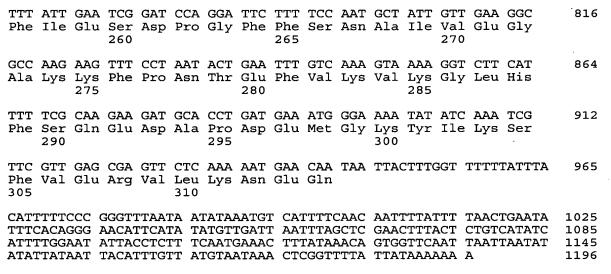
SEQUENCE LISTING

+t,1700

- (1) GENERAL INFORMATION
- (i) APPLICANT: Bryan, Bruce
- (ii) TITLE OF THE INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Brown, Martin, Haller & McClain
 - (B) STREET: 1660 Union Street
 - (C) CITY: San Diego
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 92101-2926
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 11-25-96
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/597,274
 - (B) FILING DATE: 02-06-96
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Seidman, Stephanie L
 - (B) REGISTRATION NUMBER: 33,779
 - (C) REFERENCE/DOCKET NUMBER: 6680-105
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 619-238-0999
 - (B) TELEFAX: 619-238-0062
 - (C) TELEX:
 - (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...942
 - (D) OTHER INFORMATION: Renilla Reinformis Luciferase
- (x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155





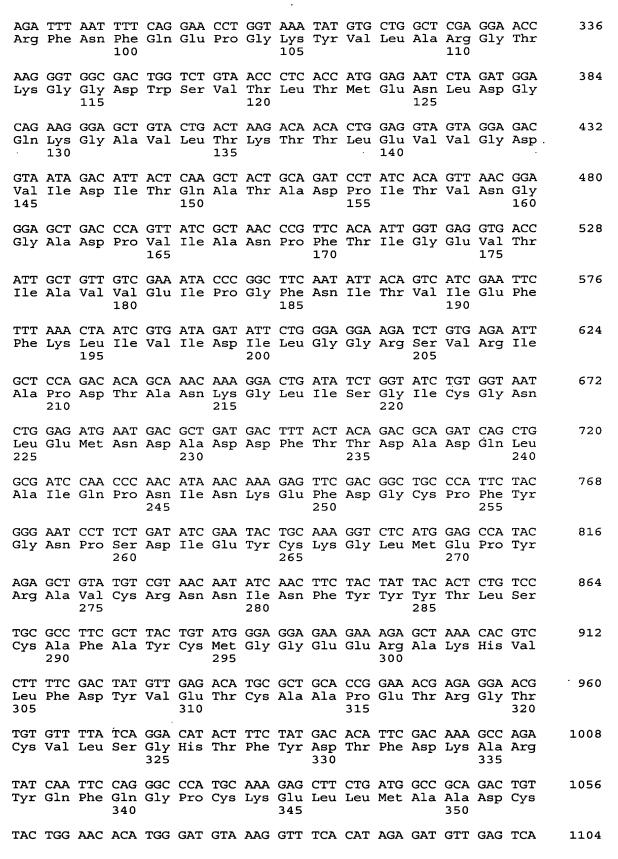
(2) INFORMATION FOR SEQ ID NO:2:

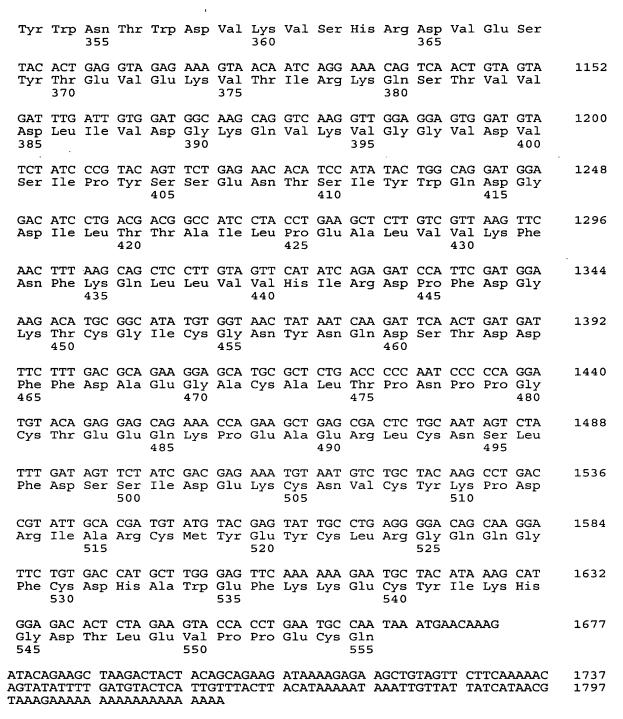
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1821 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...1665
 - (D) OTHER INFORMATION: Cypridina hilgendorfii luciferase
- (x) PUBLICATION INFORMATION:

PATENT NO.: EP 0 387 355 TORAY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAG Lys	-		_							48
TGC Cys		 	 		 		 			96
ACA Thr										144
AGA Arg 50										192
AAT Asn										240
TCC Ser			-	-		-		_		288





(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1643 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

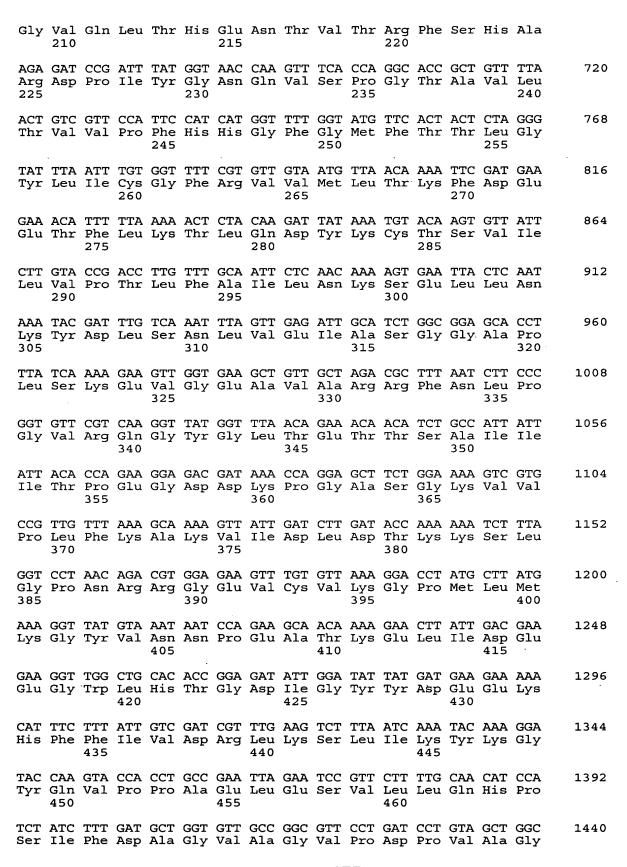
- (A) NAME/KEY: Coding Sequence(B) LOCATION: 1...1644(D) OTHER INFORMATION: Luciola Cruciata Luciferase (Firefly)

(x) PUBLICATION INFORMATION:

PATENT NO.: 4,968,613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

	Asn Met G	BAA AAC GA Blu Asn As 5							48
		AA GAG GG lu Glu Gl							96
ATG GAG C Met Glu A 3					la Phe				144
ACT GGT G Thr Gly V 50		AT TCT TA yr Ser Ty 55							192
		TG CAA AA eu Gln As 70			al Val		Arg 1		240
GCG TTA T Ala Leu C	Cys Ser G								288
GGA CTG T Gly Leu P				a Pro Tl					336
TTA CGT G Leu Arg G 1					er Lys				384
TTT AGT T Phe Ser S 130			ı Asp Lys						432
GTA ACT A Val Thr T 145				e Leu As			Asp 7		480
CGA GGA T Arg Gly T	yr Gln C								528
GGT TTT C Gly Phe G				val G					576
CAA GTT G Gln Val A 1					er Thr				624
GGC GTA C	CAA CTT A	CT CAC GA	A AAT AC	A GTC A	CT AGA	TTT TCT	CAT C	GCT	672



465				470			475			480	
		 	GCC Ala 485		 		 				1488
			ATG Met								1536
		 	GGT Gly		 		 	 	 		1584
			GAC Asp								1632
	C GCT L Ala	 				`					1644

- (2) INFORMATION FOR SEQ ID NO:4:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1819 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence

 - (B) LOCATION: 1...1664
 (D) OTHER INFORMATION: Vargula (cypridina) luciferase
- (x) PUBLICATION INFORMATION:
 - JP 3-30678 Osaka (Tsuji)

 - (A) Thompson <u>et al.</u>
 (C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
 - (D) VOLUME: 86
 - (F) PAGES: 1326-1332 (G) DATE: (1989)

 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

					CTG Leu											48
					TGT Cys											96
		-			TCT Ser		_			_						144
ACC	AGA	TGC	GCA	ACA	тст	AAA	CGA	GAT	АТА	СТА	TCA	GAT	GGA	СТС	TGT	192

55 60 GAA AAT AAA CCA GGG AAG ACA TGC TGT AGA ATG TGC CAG TAT GTG ATT 240

Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys

Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile

-176-

65	70	75	80
		TT AGA ACG TTT TAC GGO ne Arg Thr Phe Tyr Gly 95	
		AT GTG CTG GCT AGG GGA yr Val Leu Ala Arg Gly 110	
		CC ATG GAG AAT CTA GAT nr Met Glu Asn Leu Asp 125	
		CA CTG GAG GTT GCA GGA nr Leu Glu Val Ala Gly 140	
		AT CCT ATC ACA GTT AAC sp Pro Ile Thr Val Asr 155	
	Ile Ala Asn Pro Ph	TC ACA ATT GGT GAG GTO ne Thr Ile Gly Glu Val 70 175	Thr
		AT ATC ACA GTC ATC GAR sn Ile Thr Val Ile Glu 190	
		GA GGA AGA TCT GTC AGA ly Gly Arg Ser Val Arg 205	
		TA TCT GGT ATC TGT GGT le Ser Gly Ile Cys Gly 220	
		CT ACA GAT GCA GAT CAC nr Thr Asp Ala Asp Glr 235	
		TC GAC GGC TGC CCA TTC ne Asp Gly Cys Pro Phe 50 255	Tyr
		AA GGT CTG ATG GAG CCA ys Gly Leu Met Glu Pro 270	
		TC TAC TAT TAC ACT CTA ne Tyr Tyr Thr Leu 285	
		AA GAA AGA GCT AAA CAC Lu Glu Arg Ala Lys His 300	
		CG CCG GAA ACG AGA GGA la Pro Glu Thr Arg Gly 315	
		AC ACA TTC GAC AAA GCA Sp Thr Phe Asp Lys Ala 30 335	Arg

									Ile	CTG Leu					1056
								Val		CAT His					1104
										AAA Lys					1152
										GTT Val 395					1200
										ATA Ile					1248
									Glu	GCT Ala					1296
										AGA Arg					1344
										CAA Gln					1392
										ACC Thr 475					1440
										CGA Arg					1488
TTT (Asn						1536
CGG A	Ile A	Ala A	Arg (Cys I	Met :	Tyr (Glu '	Tyr	Cys		Arg (Gly (Gln (1584
TTT T					Trp (Glu					1632
GGA (Gly 1 545				Glu V							TAA Z	ACGT	ACAA	AG	1677
	TAT:	TT T	ATGT	ACTC	A TTC	STTT									1737 1797 1819

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 958 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence (B) LOCATION: 115...702

 - (D) OTHER INFORMATION: apoaequorin-encoding gene
- (x) PUBLICATION INFORMATION:

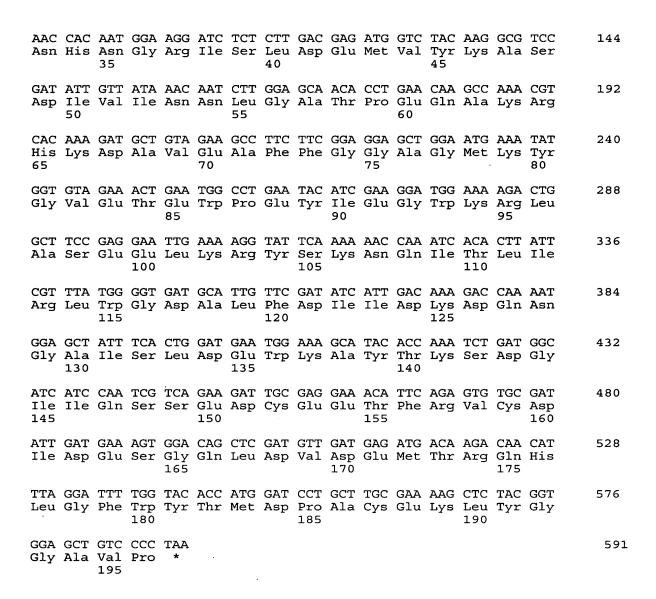
PATENT NO.: 5,093,240

(A) Inouye et al.

- (C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
- (D) VOLUME: 82
- (F) PAGES: 3154-3158 (G) DATE: (1985)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

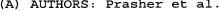
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TTACATCAAA TCTC	TAGTTG ATCAAC	CTAAA TTGTCTCGAC	AACAACAAGC AAAC	ATG 117 Met 1
		AAG CTT ACA TCA Lys Leu Thr Ser 10		
		CAT ATG TTC AAT His Met Phe Asn 25		
		GAC GAG ATG GTC Asp Glu Met Val		
		GCA ACA CCT GAG Ala Thr Pro Glu 60		
		TTC GGA GGA GCT Phe Gly Gly Ala 75		
		TAT ATT GAA GGA Tyr Ile Glu Gly 90		
		GCC AAA AAC GAA Ala Lys Asn Glu 105		
		GAT ATC GTT GAC Asp Ile Val Asp		

	115					120					125					
									TAC Tyr							549
									ACA Thr 155							597
									GAG Glu							645
									TGC Cys		-					693
	GTC Val 195		TAAC	GAAG(CTC :	racg(GTGG:	rg <i>i</i>	ATGC/	ACCC	ra go	GAAG	ATGA:	r GT	GATTTTGA	752
TGTT AGA	GAT?	TTT T	TGTAI	ATTA SAAA	GG A	ACAGA FAAAA	ATTA AAAA	A ATO	GAA:	rgat	TAG	TGT:	CTT :	TTTA	CGTTTG ATCAAC AAAAAA	812 872 932 958
		(2)	INI	FORM	OITA	1 FOI	R SE	Q ID	NO : 6	5:						
	()	(A) (B) (C)	LENG TYPE STRA	GTH: E: nu ANDEI	CHARA 591 acle: ONESS	base ic ac S: s:	e pai cid ingle	irs								
	i) i) r) r)	iii) Lv) <i>I</i> /) FI	HYPO ANTIS RAGMI ORIG	OTHE: SENSI ENT : INAL	TYPI FICAI E: NO FYPE SOUI	: NO										
		(B)	LO	CATIO	EY: (ON: 1 INFOR	L5	588	•	nce ombir	nant	Aeqı	orii	n AE(Q1		
	()	c) PU	BLI	CATIO	II NO	VFORM	OITAN	ON:								
		(B) (C) (D) (F)	JOU VOI PAC	TLE: DNAs JRNAI LUME:	Enco L: Bi : 26	ence oding loche	e Com g Aec emist	mpari quori	isons in Is			oleme	entai	ry		
	(2	ci) S	EQUE	ENCE	DESC	CRIPT	CION:	: SEÇ	O ID	NO : 6	5:					
									CTT Leu 10							48
									ATG Met							96



(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 591 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...588
 - (D) OTHER INFORMATION: Recombinant Aequorin AEQ2
- (x) PUBLICATION INFORMATION:



- (A) AUTHORS: Prasher et al.
 (B) TITLE: Sequence Comparisons of Complementary
 DNAs Encoding Aequorin Isotypes
 (C) JOURNAL: Biochemistry
 (D) VOLUME: 26
 (F) PAGES: 1326-1332
 (G) DATE: 1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

				_	AAG Lys			_			4	8
 -					CAT His 25					_	9	6
					GAC Asp						. 14	4
					GCA Ala						19	2
					TTC Phe						24	0
 					TAT Tyr						28	8
					GCC Ala 105		_				33	6
					GAT Asp						38	4
					AAA Lys				_	_	43	2
					GAG Glu						48	0
					GTT Val						52	8
					CCT Pro 185					_	57	6
 GCT Ala	_	TAA *									5	91

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 591 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence (B) LOCATION: 1...588

 - (D) OTHER INFORMATION: Recombinant Aequorin AEQ3

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Prasher et al.
- (B) TITLE: Sequence Comparisons of Complementary DNAs Encoding Aequorin Isotypes
- (C) JOURNAL: Biochemistry
 (D) VOLUME: 26
- (F) PAGES: 1326-1332
- (G) DATE: 1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

			TCA Ser					48
 		 	CAC His					96
			TCT Ser					144
			CTT Leu 55					192
			GAC Asp					240
 			CCT Pro					288
			AAA Lys					336
 	 	 	TTG Leu	 	 			384
 			GAA Glu					432

130			135			140			
ATC Ile									480
 GAT Asp	 		 	 	 		 	 	528
 GGA Gly	 		 	 	 		 	 	576
 GCT Ala	 	TAA *							591

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 567 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...567

 - (D) OTHER INFORMATION: Aequorin photoprotein

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Charbonneau et al.
- (B) TITLE: Amino acid sequence of the calcium-dependent photoprotein aequorin
- (C) JOURNAL: Am. Chem. Soc. (D) VOLUME: 24
- (E) ISSUE: 24
- (F) PAGES: 6762-6771
- (G) DATE: 1985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

			TTC Phe				 	 48
			CTT Leu	 	 	 	 	 96
			AAG Lys					144
			 GCC Ala		 	 	 	 192

	50			55			60			
_	TTC Phe									240
	TAC Tyr									288
	TCA Ser									336
	GAT Asp									384
	AAA Lys 130									432
	GAG Glu									480
	GTT Val									528
	CCT Pro	 	_							567

- (2) INFORMATION FOR SEQ ID NO:10:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...588
- (D) OTHER INFORMATION: Aequorin mutant w/increased bioluminescence activitý
 - (x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

- (K) RELEVANT RESIDUES IN SEQ ID NO: 10: Asp 124 changed to Ser
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA CCA GAC TTC GAC AAC Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn 48

1		5			10			15		
	TGG Trp									96
	AAT Asn 35									144
	GTT Val									192
	GAT Asp									240
	 GAA Glu	 	 							288
	GAG Glu									336
	TGG Trp 115									384
	ATT Ile									432
	CAA Gln									480
	GAA Glu									528
	 TTT Phe	 _			_	_				576
	GTC Val 195									588

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 588 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO

- (iv) ANTISENSE: NO (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence(B) LOCATION: 1...588(D) OTHER INFORMATION: Recombinant site-directed Aequorin mutant w/increased biolum. activity

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

(K) RELEVANT RESIDUES IN SEQ ID NO:11: Glu 135 changed to Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

				TCA Ser									48
		_		CAC His			_		_		_		96
				TCT Ser								1	.44
				CTT Leu 55								1	.92
				GCC Ala								2	40
				CCT Pro								2	88
				AGG Arg								3	36
				TTG Leu								3	84
				TCA Ser 135							_	4	:32
				GAT Asp				Phe				4	80
			_	CTC Leu							_	5	28
_	_		_	ATG Met		_		_			_	5	76
	GTC Val 195												588





(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence (B) LOCATION: 1...588

 - (D) OTHER INFORMATION: Recombinant site-directed Aequorin mutant w/increased biolum. activity
- (x) PUBLICATION INFORMATION: PATENT NO.: 5,360,728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

		TAC Tyr						48
		CGA Arg						96
		ATC Ile						144
		AAT Asn						192
		GAA Glu 70						240
		TGG Trp						288.
		AAA Lys						336
		GCA Ala						384
 	 	 GAT Asp	 	 	 	 	 	432
		GAA Glu 150						480





GAT Asp									528
 GGA Gly	 	 	 	 		 	 		576
 GCT Ala	 				,				588

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 567 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...567

 - (D) OTHER INFORMATION: Recombinant apoaequorin (AQUALITE®)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

	-						GGA Gly		48
 							AGG Arg 30		96
							AAC Asn		144
							GTA Val		192
							GAA Glu		240
							TTG Leu		288
							GAT Asp 110		336
							TCA Ser		384
							TCA Ser		432





TGC GAG GAA ACA TTC AGA GTG TGC GAT ATT GAT GAA AGT GGA CAG CTC Cys Glu Glu Thr Phe Arg 150 Val Cys Asp Ile Asp Glu Ser Gly Gln Leu 160

GAT GTT GAT GAG AGA AGA AGA CAA CAT TTA GGA TTT TGG TAC ACC ATG Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro

480

480

480

480

480

528

480

528

528

528

- (2) INFORMATION FOR SEQ ID NO:14:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 236 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (x) PUBLICATION INFORMATION: PATENT NO.: 5,484,723
- (ix) FEATURE:
 - (D) OTHER INFORMATION: Vibrio fisheri Flavin reductase
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Pro Ile Asn Cys Lys Val Lys Ser Ile Glu Pro Leu Ala Cys Asn 1 5 10 15

Thr Phe Arg Ile Leu Leu His Pro Glu Gln Pro Val Ala Phe Lys Ala 20 25 30

Gly Gln Tyr Leu Thr Val Val Met Gly Glu Lys Asp Lys Arg Pro Phe
35 40 45

Ser Ile Ala Ser Ser Pro Cys Arg His Glu Gly Glu Ile Glu Leu His 50 55 60

Ile Gly Ala Ala Glu His Asn Ala Tyr Ala Gly Glu Val Val Glu Ser 65 70 75 80

Met Lys Ser Ala Leu Glu Thr Gly Gly Asp Ile Leu Ile Asp Ala Pro 85 90 95

His Gly Glu Ala Trp Ile Arg Glu Asp Ser Asp Arg Ser Met Leu Leu 100 105 110

Ile Ala Gly Gly Thr Gly Phe Ser Tyr Val Arg Ser Ile Leu Asp His
115 120 125

Cys Ile Ser Gln Gln Ile Gln Lys Pro Ile Tyr Leu Tyr Trp Gly Gly 130 135 140

Arg Asp Glu Cys Gln Leu Tyr Ala Lys Ala Glu Leu Glu Ser Ile Ala 145 150 155 160

Gln Ala His Ser His Ile Thr Phe Val Pro Val Val Glu Lys Ser Glu 165 170 175

Gly Trp Thr Gly Lys Thr Gly Asn Val Leu Glu Ala Val Lys Ala Asp

180

DOINGORD CONTRO

185

190

Phe Asn Ser Leu Ala Asp Met Asp Ile Tyr Ile Ala Gly Arg Phe Glu 195 200

Met Ala Gly Ala Ala Arg Glu Gln Phe Thr Thr Glu Lys Gln Ala Lys 210 215

Lys Glu Gln Leu Phe Gly Asp Ala Phe Ala Phe Ile 230